

SEQUENCE LISTING

<110> Allison, Anthony

<120> MODIFIED ANNEXIN PROTEINS AND METHODS FOR TREATING VASO-OCCLUSIVE
SICKLE-CELL DISEASE

<130> SURR.113

<150> 60/400,718

<151> 2002-08-02

<150> 10/080,370

<151> 2002-02-21

<160> 9

<170> PatentIn version 3.2

<210> 1

<211> 960

<212> DNA

<213> Homo sapiens

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accgcccgtc ccaacgcccga gcgccagcag atcgccgagg agttcaagac cctgttcggc	180
cgcgacctgg tgaacgacat gaagtccgag ctgaccggca agttcgagaa gctgatcgtg	240
gccctgatga agccctcccg cctgtacgac gcctacgagc tgaagcacgc caagctgggc	300
gccggcaccg acgagaaggt gctgaccgag atcatcgctt cccgcacccc cgaggagctg	360
cgcgccatca agcaggccta cgaggaggag tacgggtcca acctggagga cgacgtggtg	420
ggcgacacct ccggctacta ccagcgcatt ctggtggtgc tgctgcaggc caaccgcgac	480
cccgaacccg ccatcgacga cgcccagggt gagctggacg cccaggccct gttccaggcc	540
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gtgtcccacc tgcgccgcgt gttcgacaag tacatgacca tctccggctt ccagatcgag	660
gagaccatcg accgcgagac ctccggcaac ctggagaacc tgctgctggc cgtggtgaag	720
tccatccgtc ccatccccgc ctacctggcc gagaccctgt actacgcat gaagggcgcc	780
ggcaccgacg accacacct gatccgcgtg atcgtgtccc gctccgagat cgacctgttc	840
aacatccgca aggagttccg caagaacttc gccacctccc tgtactccat gatcaagggc	900

gacacctccg gcgactacaa gaaggccctg ctgctgctgt gcggcggcga ggacgactga 960

<210> 2
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(960)

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 Met Ala Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg
 1 5 10 15
 gcc gac gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac 96
 Ala Asp Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp
 20 25 30
 gag gac tcc atc ctg aac ctg ctg acc gcc cgc tcc aac gcc cag cgc 144
 Glu Asp Ser Ile Leu Asn Leu Thr Ala Arg Ser Asn Ala Gln Arg
 35 40 45
 cag cag atc gcc gag gag ttc aag acc ctg ttc ggc cgc gac ctg gtg 192
 Gln Gln Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val
 50 55 60
 aac gac atg aag tcc gag ctg acc ggc aag ttc gag aag ctg atc gtg 240
 Asn Asp Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val
 65 70 75 80
 gcc ctg atg aag ccc tcc cgc ctg tac gac gcc tac gag ctg aag cac 288
 Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His
 85 90 95
 gcc aag ctg ggc gcc ggc acc gac gag aag gtg ctg acc gag atc atc 336
 Ala Lys Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile
 100 105 110
 gcc tcc cgc acc ccc gag gag ctg cgc gcc atc aag cag gcc tac gag 384
 Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu
 115 120 125
 gag gag tac ggc tcc aac ctg gag gac gac gtg gtg ggc gac acc tcc 432
 Glu Glu Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser
 130 135 140
 ggc tac tac cag cgc atg ctg gtg gtg ctg ctg cag gcc aac cgc gac 480
 Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp
 145 150 155 160
 ccc gac acc gcc atc gac gac gcc cag gtg gag ctg gac gcc cag gcc 528
 Pro Asp Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala

165	170	175	
ctg ttc cag gcc ggc gag ctg aag tgg ggc acc gac gag gag aag ttc			576
Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe			
180	185	190	
atc acc atc ctg ggc acc cgc tcc gtg tcc cac ctg cgc cgc gtg ttc			624
Ile Thr Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe			
195	200	205	
gac aag tac atg acc atc tcc ggc ttc cag atc gag gag acc atc gac			672
Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp			
210	215	220	
cgc gag acc tcc ggc aac ctg gag aac ctg ctg ctg gcc gtg gtg aag			720
Arg Glu Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys			
225	230	235	240
tcc atc cgc tcc atc ccc gcc tac ctg gcc gag acc ctg tac tac gcc			768
Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala			
245	250	255	
atg aag ggc gcc ggc acc gac gac cac acc ctg atc cgc gtg atc gtg			816
Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val			
260	265	270	
tcc cgc tcc gag atc gac ctg ttc aac atc cgc aag gag ttc cgc aag			864
Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys			
275	280	285	
aac ttc gcc acc tcc ctg tac tcc atg atc aag ggc gac acc tcc gcc			912
Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly			
290	295	300	
gac tac aag aag gcc ctg ctg ctg ctg tgc ggc ggc gag gac gac tga			960
Asp Tyr Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp			
305	310	315	

<210> 3

<211> 319

<212> PRT

<213> Homo sapiens

<400> 3

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		20						25					30		

Glu	Asp	Ser	Ile	Leu	Asn	Leu	Leu	Thr	Ala	Arg	Ser	Asn	Ala	Gln	Arg
		35					40					45			

Gln Gln Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val
 50 55 60

Asn Asp Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val
 65 70 75 80

Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His
 85 90 95

Ala Lys Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile
 100 105 110

Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu
 115 120 125

Glu Glu Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser
 130 135 140

Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp
 145 150 155 160

Pro Asp Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala
 165 170 175

Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe
 180 185 190

Ile Thr Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe
 195 200 205

Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp
 210 215 220

Arg Glu Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys
 225 230 235 240

Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala
 245 250 255

Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val
 260 265 270

Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys
 275 280 285

Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly
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Asp Tyr Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp
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<210> 4
 <211> 2016
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

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<220>
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 <222> (1000)..(1002)
 <223> n = a, c, t, or g

<220>
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 <222> (1051)..(1053)
 <223> n = a, c, t, or g

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 aagggcctgg gcaccgacga ggactccatc ctgaacctgc tgaccgcccg ctccaacgcc 180
 cagcgccagc agatcgccga ggagttcaag accctgttcg gccgcgacct ggtgaacgac 240
 atgaagtccg agctgaccgg caagttcgag aagctgatcg tggccctgat gaagccctcc 300
 cgctgttacg acgcctacga gctgaagcac gccaaagtgg gcgccggcac cgacgagaag 360
 gtgctgaccg agatcatcgc ctcccgacc cccgaggagc tgcgcgccat caagcaggcc 420
 tacgaggagg agtacggctc caacctggag gacgacgtgg tgggcgacac ctccggctac 480
 taccagcgca tgctggtggt gctgctgcag gccaaaccgcg accccgacac cgccatcgac 540
 gacgccaggg tggagctgga cgcccaggcc ctgttccagg ccggcgagct gaagtggggc 600

accgacgagg	agaagttcat	caccatcctg	ggcaccgcgt	ccgtgtccca	cctgcgccgc	660
gtgttcgaca	agtacatgac	catctccggc	ttccagatcg	aggagaccat	cgaccgcgag	720
acctccggca	acctggagaa	cctgctgctg	gccgtggtga	agtccatccg	ctccatcccc	780
gcctacctgg	ccgagaccct	gtactacgcc	atgaagggcg	ccggcaccga	cgaccacacc	840
ctgatccgcg	tgatcgtgtc	ccgctccgag	atcgacctgt	tcaacatccg	caaggagttc	900
cgcaagaact	tcgccacctc	cctgtactcc	atgatcaagg	gcgacacctc	cggcgactac	960
aagaaggccc	tgctgctgct	gtgcggcggc	gaggacgacn	nnagatctcg	atcggggcctg	1020
gaggtgctgt	tccagggccc	cggaagtact	nnngccctgc	gcggcaccgt	gaccgacttc	1080
tccggcttcg	acggccgcgc	cgacgccgag	gtgctgcgca	aggccatgaa	gggcctgggc	1140
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atcgccgagg	agttcaagac	cctgttcggc	cgcgacctgg	tgaacgacat	gaagtccgag	1260
ctgaccggca	agttcgagaa	gctgatcgtg	gccctgatga	agccctcccg	cctgtacgac	1320
gcctacgagc	tgaagcacgc	caagctgggc	gccggcaccg	acgagaaggt	gctgaccgag	1380
atcatcgcc	cccgcacccc	cgaggagctg	cgcgccatca	agcaggccta	cgaggaggag	1440
tacggctcca	acctggagga	cgacgtggtg	ggcgacacct	ccggctacta	ccagcgcatg	1500
ctggtggtgc	tgctgcaggc	caaccgcgac	cccgcacccg	ccatcgacga	cgcccagggtg	1560
gagctggacg	cccaggccct	gttccaggcc	ggcgagctga	agtggggcac	cgacgaggag	1620
aagttcatca	ccatcctggg	caccgcgtcc	gtgtcccacc	tgcgccgcgt	gttcgacaag	1680
tacatgacca	tctccggctt	ccagatcgag	gagaccatcg	accgcgagac	ctccggcaac	1740
ctggagaacc	tgctgctggc	cgtggtgaag	tccatccgct	ccatccccgc	ctacctggcc	1800
gagaccctgt	actacgccat	gaagggcgcc	ggcaccgacg	accacaccct	gatccgcgtg	1860
atcgtgtccc	gctccgagat	cgacctgttc	aacatccgca	aggagttccg	caagaacttc	1920
gccacctccc	tgtactccat	gatcaagggc	gacacctccg	gcgactacaa	gaaggccctg	1980
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<210> 5
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

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<220>
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<220>
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 <223> n = a, c, t, or g

<220>
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 <223> n = a, c, t, or g

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ctg cgc ggc acc gtg acc gac ttc tcc ggc ttc gac ggc cgc gcc gac	96
Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp	
20 25 30	
gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac gag gac	144
Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp	
35 40 45	
tcc atc ctg aac ctg ctg acc gcc cgc tcc aac gcc cag cgc cag cag	192
Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln	
50 55 60	
atc gcc gag gag ttc aag acc ctg ttc ggc cgc gac ctg gtg aac gac	240
Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp	
65 70 75 80	
atg aag tcc gag ctg acc ggc aag ttc gag aag ctg atc gtg gcc ctg	288
Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu	
85 90 95	
atg aag ccc tcc cgc ctg tac gac gcc tac gag ctg aag cac gcc aag	336
Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys	
100 105 110	
ctg ggc gcc ggc acc gac gag aag gtg ctg acc gag atc atc gcc tcc	384
Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser	
115 120 125	
cgc acc ccc gag gag ctg cgc gcc atc aag cag gcc tac gag gag gag	432
Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu	
130 135 140	

tac ggc tcc aac ctg gag gac gac gtg gtg ggc gac acc tcc ggc tac	480
Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr	
145 150 155 160	
tac cag cgc atg ctg gtg gtg ctg ctg cag gcc aac cgc gac ccc gac	528
Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp	
165 170 175	
acc gcc atc gac gac gcc cag gtg gag ctg gac gcc cag gcc ctg ttc	576
Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe	
180 185 190	
cag gcc ggc gag ctg aag tgg ggc acc gac gag gag aag ttc atc acc	624
Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr	
195 200 205	
atc ctg ggc acc cgc tcc gtg tcc cac ctg cgc cgc gtg ttc gac aag	672
Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys	
210 215 220	
tac atg acc atc tcc ggc ttc cag atc gag gag acc atc gac cgc gag	720
Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu	
225 230 235 240	
acc tcc ggc aac ctg gag aac ctg ctg ctg gcc gtg gtg aag tcc atc	768
Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile	
245 250 255	
cgc tcc atc ccc gcc tac ctg gcc gag acc ctg tac tac gcc atg aag	816
Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys	
260 265 270	
ggc gcc ggc acc gac gac cac acc ctg atc cgc gtg atc gtg tcc cgc	864
Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg	
275 280 285	
tcc gag atc gac ctg ttc aac atc cgc aag gag ttc cgc aag aac ttc	912
Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe	
290 295 300	
gcc acc tcc ctg tac tcc atg atc aag ggc gac acc tcc ggc gac tac	960
Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr	
305 310 315 320	
aag aag gcc ctg ctg ctg ctg tgc ggc ggc gag gac gac nnn aga tct	1008
Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp Xaa Arg Ser	
325 330 335	
cga tcg ggc ctg gag gtg ctg ttc cag ggc ccc gga agt act nnn gcc	1056
Arg Ser Gly Leu Glu Val Leu Phe Gln Gly Pro Gly Ser Thr Xaa Ala	
340 345 350	
ctg cgc ggc acc gtg acc gac ttc tcc ggc ttc gac ggc cgc gcc gac	1104
Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp	
355 360 365	
gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac gag gac	1152

Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp	
370 375 380	
tcc atc ctg aac ctg ctg acc gcc cgc tcc aac gcc cag cgc cag cag	1200
Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln	
385 390 395 400	
atc gcc gag gag ttc aag acc ctg ttc ggc cgc gac ctg gtg aac gac	1248
Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp	
405 410 415	
atg aag tcc gag ctg acc ggc aag ttc gag aag ctg atc gtg gcc ctg	1296
Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu	
420 425 430	
atg aag ccc tcc cgc ctg tac gac gcc tac gag ctg aag cac gcc aag	1344
Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys	
435 440 445	
ctg ggc gcc ggc acc gac gag aag gtg ctg acc gag atc atc gcc tcc	1392
Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser	
450 455 460	
cgc acc ccc gag gag ctg cgc gcc atc aag cag gcc tac gag gag gag	1440
Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu	
465 470 475 480	
tac ggc tcc aac ctg gag gac gac gtg gtg ggc gac acc tcc ggc tac	1488
Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr	
485 490 495	
tac cag cgc atg ctg gtg gtg ctg ctg cag gcc aac cgc gac ccc gac	1536
Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp	
500 505 510	
acc gcc atc gac gac gcc cag gtg gag ctg gac gcc cag gcc ctg ttc	1584
Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe	
515 520 525	
cag gcc ggc gag ctg aag tgg ggc acc gac gag gag aag ttc atc acc	1632
Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr	
530 535 540	
atc ctg ggc acc cgc tcc gtg tcc cac ctg cgc cgc gtg ttc gac aag	1680
Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys	
545 550 555 560	
tac atg acc atc tcc ggc ttc cag atc gag gag acc atc gac cgc gag	1728
Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu	
565 570 575	
acc tcc ggc aac ctg gag aac ctg ctg ctg gcc gtg gtg aag tcc atc	1776
Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile	
580 585 590	
cgc tcc atc ccc gcc tac ctg gcc gag acc ctg tac tac gcc atg aag	1824
Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys	

595	600	605	
ggc gcc ggc acc gac gac cac acc ctg atc cgc gtg atc gtg tcc cgc			1872
Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg			
610	615	620	
tcc gag atc gac ctg ttc aac atc cgc aag gag ttc cgc aag aac ttc			1920
Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe			
625	630	635	640
gcc acc tcc ctg tac tcc atg atc aag ggc gac acc tcc ggc gac tac			1968
Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr			
645	650	655	
aag aag gcc ctg ctg ctg ctg tgc ggc ggc gag gac gac taa taa taa			2016
Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp			
660	665		

<210> 6
 <211> 669
 <212> PRT
 <213> Artificial Sequence

<220>
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 <222> (15)..(15)
 <223> The 'Xaa' at location 15 stands for Ser.

<220>
 <221> misc_feature
 <222> (334)..(334)
 <223> The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>
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 <222> (351)..(351)
 <223> The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>
 <223> primer

<400> 6

Met	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Leu	Ala	Ala	Ala	Asn	Xaa	Ala
1				5					10					15	

Leu	Arg	Gly	Thr	Val	Thr	Asp	Phe	Ser	Gly	Phe	Asp	Gly	Arg	Ala	Asp
			20					25					30		

Ala	Glu	Val	Leu	Arg	Lys	Ala	Met	Lys	Gly	Leu	Gly	Thr	Asp	Glu	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln		
50	55	60
Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp		
65	70	75
Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu		
	85	90
Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys		
	100	105
Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser		
	115	120
Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu		
	130	135
Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr		
145	150	155
Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp		
	165	170
Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe		
	180	185
Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr		
	195	200
Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys		
	210	215
Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu		
225	230	235
Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile		
	245	250
Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys		
	260	265
		270

Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg
275 280 285

Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe
290 295 300

Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr
305 310 315 320

Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp Xaa Arg Ser
325 330 335

Arg Ser Gly Leu Glu Val Leu Phe Gln Gly Pro Gly Ser Thr Xaa Ala
340 345 350

Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp
355 360 365

Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp
370 375 380

Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln
385 390 395 400

Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp
405 410 415

Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu
420 425 430

Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys
435 440 445

Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser
450 455 460

Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu
465 470 475 480

Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr
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Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp
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Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe
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Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr
530 535 540

Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys
545 550 555 560

Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu
565 570 575

Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile
580 585 590

Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys
595 600 605

Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg
610 615 620

Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe
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Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr
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Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp
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